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FIGURE 338

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSSS
QPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPYSC
SVNVQDKQKGSRGHSIKTLELNVLPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQWDR
QLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPAAVVAG
AVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTLSSVTS
ARALRPPHGFPRPGALTPTPSLSSQALPSPRLPTTDGAHPQIPISPIPGGVSSSGLSRMGAVPV
MVPAQSQAGSLV

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

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FIGURE 339

GCGAGAACCTTTGACGCGGCACAACTACGGGGACGATTTCTGATTGATTTTGGCGCTTTCGATCCACCCCTCCT
 CCTTTCTC**ATG**GGACTTTGGGGACAAAGCGTCCCGACCGCCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGCCA
 GGACAGCGTCGGGAACACAGACCATGGCTCCTGGACCCCAAGATCCTTAAGTTCTGTCGTCTTCATCGTCGCGGTTT
 TGCTGCCGGTCCGGTTGACTCTGCCACCATCCCCGGCAGGACGAAGTTCCCGAGCAGACAGTGGCCCCACAGC
 AACAGAGGCGCAGCCTCAAGGAGGAGGAGTGTCAGCAGGATCTCATAGATCAGAATATACTGGAGCCTGTAACC
 CGTGCACAGAGGGTGTGGATTACACCATTGCTTCCAACAATTTGCCTTCTTGCCTGCTATGTACAGTTTGTAAAT
 CAGGTCAAACAAATAAAAGTTCTGTACCACGACAGAGACACCGTGTGTCAAGTGTGAAAAAGGAAGCTTCCAGG
 ATAAAAACTCCCCTGAGATGTGCCGGACGTGTAGAACAGGGTGTCCAGAGGGATGGTCAAGGTCAAGTAAATGTA
 CGCCCCGGAGTGACATCAAGTGCAAAAATGAATCAGCTGCCAGTTCCACTGGGAAAACCCAGCAGCGGAGGAGA
 CAGTGACCAACCATCTTGGGGATGCTTGCCTCTCCCTATCACTACCTTATCATCATAGTGGTTTTAGTCATCATTT
 TAGCTGTGGTTGTGGTTGGCTTTTCATGTGGAAGAAATTCATTTCTTACCTCAAAGGCATCTGCTCAGGTGGTG
 GAGGAGGTCCCGAACGTGTGCACAGAGTCTTTTCCGGCGGCGTTTCATGTCTTTCAGAGTTCTTGGGGCGGAGG
 ACAATGCCCGCAACGAGACCTGAGTAACAGATACTTGCAGCCACCCAGGTCTCTGAGCAGGAAATCCAAGGTC
 AGGAGCTGGCAGAGCTAACAGGTGTGACTGTAGAGTGGCCAGAGGAGCCACAGCGTCTGCTGGAACAGGCAGAAG
 CTGAAGGGTGTGAGAGGAGGAGCTGCTGGTTCCAGTGAATGACGCTGACTCCGCTGACATCAGCACCTTGCTGG
 ATGCCTCGGCAACACTGGAAGAAGGACATGCAAAGGAACAATTCAGGACCAACTGGTGGGCTCCGAAAAGCTCT
 TTTATGAAGAAGATGAGGCAGGCTCTGCTACGTCTGCTGTGAAGAATCTCTTCAGGAAACCAGAGCTTCCCT
 CATTTACCTTTTCTCTACAAAGGGAAGCAGCCTGGAAGAAACAGTCCAGTACTTGACCCATGCCCAACAACT
 CTACTATCCAATATGGGGCAGCTTACCAATGGTCTTAGAATTTGTTAACGCACTTGGAGTAATTTTATGAAT
 ACTGCGTGTGATAAGCAACCGGGAGAAATTTATATCAGATTCTTGGCTGCATAGTTATACGATTGTGTATTAAGG
 GTCGTTTTAGGCCACATGCGGTGGCTCATGCCGTGAATCCAGCACTTTGATAGGCTGAGGCAGGTGGATTGCTT
 GAGCTCGGGAGTTTGAGACCAGCTCATCAACACAGTGAACTCCATCTCAATTTAAAAAGAAAAAAGTGGTTT
 TAGGATGTCAATCTTTGCAGTTCTTCATCATGAGACAAGTCTTTTTTTCTGCTTCTTATATTGCAAGCTCCATCT
 CTACTGGTGTGTGCATTTAATGACATCTAATACAGATGCCGCACAGCCACAATGCTTTGCCTTATAGTTTTTTA
 ACTTTAGAACGGGATTATCTTGTATTACCTGTATTTTCAGTTTCCGATATTTTGACTTAATGATGAGATTATC
 AAGACGTAGCCCTATGCTAAGTCATGAGCATATGGACTTACGAGGGTTCGACTTAGAGTTTTGAGCTTTAAGATA
 GGATTATTGGGGCTTACCCCACTTAATTAGAGAAACATTTATATTGCTTACTACTGTAGGCTGTACATCTCTT
 TTCGATTTTTGTATAATGATGTAAACATGGAAAAACTTTAGGAAATGCACTTATTAGGCTGTTTACATGGGTTG
 CCTGGATACAAATCAGCAGTCAAAAATGACTAAAAATATACTAGTGACGGAGGGAGAAATCCTCCCTCTGTGGG
 AGGCACTTACTGCATTCCAGTTCTCCCTCCTGCGCCCTGAGACTGGACCAGGGTTTGATGGCTGGCAGCTTCTCA
 AGGGGCAGCTTGTCTTACTTGTAAATTTTAGAGGTATATAGCCATATTTATTTATAAATAAATATTTATTTATTT
 ATTTATAAGTAGATGTTTACATATGCCAGGATTTTGAAGAGCCTGGTATCTTTGGGAAGCCATGTGTCTGGTTT
 GTCGTGCTGGGACAGTCATGGGACTGCATCTTCCGACTTGTCCACAGCAGATGAGGACAGTGAGAATTAAGTTAG
 ATCCGAGACTGCCAAGAGCTTCTCTTCAAGCGCCATTACAGTTGAACGTTAGTGAATCTTGAGCCTCATTTGGG
 CTCAGGGCAGAGCAGGTGTTTATCTGCCCGGCATCTGCCATGGCATCAAGAGGGAAGAGTGGACGGTGTCTGGG
 AATGGTGTGAAATGGTTGCCGACTCAGGCATGGATGGGCCCTCTCGCTTCTGGTGGTCTGTGAACCTGAGTCCCT
 GGGATGCCCTTTAGGGCAGAGATTCTTGAGCTGCGTTTTAGGGTACAGATTCCCTGTTTGAGGAGCTTGGCCCT
 CTGTAAGCATCTGACTCATCTCAGAGATATCAATTTCTAAACACTGTGACAACGGGATCTAAAATGGCTGACACA
 TTTGTCTTGTGTACGTTCCATTATTTTATTTAAAAACCTCAGTAATCGTTTTAGCTTCTTTCCAGCAAACTCT
 TCTCCACAGTAGCCAGTCGTGGTAGGATAAATTACGGATATAGTCATTTAGGGGTTTCAGTCTTTCCATCTC
 AAGGCATTGTGTGTTTTGTCCGGGACTGGTTTGGCTGGGACAAAGTTAGAACTGCCTGAAGTTCCGCACATTCAG
 ATTGTTGTGTCCATGGAGTTTTAGGAGGGGATGGCCCTTCCGGTCTTCGCACTTCCATCCTCTCCCACTTCCATC
 TGGCGTCCACACCTTGTCCCTGCACTTCTGGATGACACAGGGTGTGCTGCCTCCTAGTCTTTGCCTTTGCTG
 GGCTTCTGTGCAGGAGACTTGGTCTCAAGCTCAGAGAGAGCCAGTCCGGTCCAGCTCCTTTGTCCCTTCCCTC
 AGAGGCTTCTTTGAAGATGCATCTAGACTACCAGCCTTATCAGTGTTTAAGCTTATTCCTTTAACATAAGCTTC
 CTGACAACATGAAATTTGTTGGGGTTTTTGGCGTTGGTTGATTTGTTTAGGTTTTGCTTTATACCCGGGCCAAAT
 AGCACATAACACCTGGTTATATATGAAATACTCATATGTTTATGACCAAAATAAATATGAAACCTCATRTTAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 340

MGLWGQSVPTASSARAGRYPGARTASGTRFWLLDPKILKFVVFIVAVLLPVRVDSATIPRQDEVPPQTVAPQQQR
RSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSGQTNKSSCTTTRDTVCQCEKGSFQDKN
SPEMCRTCRTGCFRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAEETVTTILGMLASPYHYLIIIVVLVIIILAV
VVVGFSCKKKFISYLKGICSGGGGGPERVHRVLFRRRSCPSRVGAEDNARNETLSNRYLQPTQVSEQEIQGQEL
AELTGVTVESPEEPQRLLEQAEAGCQRRRLLVFVNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKLFYE
EDEAGSATSC

Important features:**Transmembrane domains:**

amino acids 35-52, 208-230

N-glycosylation sites.

amino acids 127-131, 182-186, 277-281

Glycosaminoglycan attachment site.

amino acids 245-249

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 260-264

N-myristoylation sites.

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276, 297-303, 380-386

ATP/GTP-binding site motif A (P-loop).

amino acids 185-193

TNFR/NGFR cysteine-rich region.

amino acids 99-139

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FIGURE 341

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAGG
CCATGCTTCGTTTCTTGCCAGATTTGGCTTTCAGCTTCCTGTAAATTCTGGCTTTGGGCCAGG
CAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTTCACCCC
AGAAGTTCCAACCTGTGCCTTATATCTTGAAGAAAATTTTCCAGGATCGCGAGGCAGCAGCGA
CCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGGAATGTACTTC
GCTTTCTCCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCTCCTGCC
TGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACATTGGCCC
AGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGAAGTGGCTC
TGTTCTGTTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTAAAATGTTTG
TGTTGCGGTCACTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGATGTAGCTAAGG
ATTGGAATGACAACCCCCGGAAAAATTTGCGGTTATTCCTGGAGATACTGGTCAAAGAAGATA
GAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGATGCTCCCTTCATG
CTTCCCTGCTGGTGGTGACTCTCAACCCTGATCAGTGCCACCCTTCTCGGAAAAGGAGAGCAG
CCATCCCTGTCCCCAAGCTTTCTTGTAAGAACCTCTGCCACCGTCACCAGCTATTTCATTA
TCCGGGACCTGGGTTGGCACAAGTGGATCATTGCCCCCAAGGGGTTTCATGGCAAATTACTGCC
ATGGAGAGTGTCCCTTCTCACTGACCATCTCTCTCAACAGCTCCAATTATGCTTTCATGCAAG
CCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTGTATCCCCACCAAGCTGTCTC
CCATTTCCATGCTCTACCAGGACAATAATGACAATGTCATTCTACGACATTATGAAGACATGG
TAGTCGATGAATGTGGGTGTGGGTAGGATGTCAGAAATGGGAATAGAAGGAGTGTCTTAGGG
TAAATCTTTTAATAAAACTACCTATCTGGTTTATGACCACTTAGATCGAAATGTC

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FIGURE 342

MLRFLPDLAFSFLLILALGQAVQFQEYVFLQFLGLDKAPSPQKFQPVPIILKKIFQDREAAAT
TGVSRLCYVKELGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQ
LGLDLGPNSYYNLGPELELALFLVQEPHVWGQTPKPGKMFVLRVWPWPQGAVHENLLDVAKD
WNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTNLNPDQCHPSRKRRAA
IPVPKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYPCHGECFSLTISLNSSNYAFMQA
LMHAVDPEIPQAVCIPTKLSPISMPLYQDNNDNVILRHYEDMVVDECGCG

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 112-116, 306-310

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 96-100

N-myristoylation site.

amino acids 77-83

TGF-beta family proteins.

amino acids 264-299, 327-341, 345-364

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FIGURE 343

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCCTTTTCATTGACAACTGACTTTTTTTATTTCT
TTTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT
CTGTGTTTTGGGGTTTCTTCTCTCCCTGACATTGGCATTGCTTAGTGGTTGTGTGGGGAGGGAGACCACGTGG
GCTCAGTGCTTGCTTGCACTTATCTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTC
ATCGCTGGTGGTATCCTGGCGGCCCTTGCTCCTGCTGATAGTTGTCTGTGCTCTGTCTTTACTTCAAAATACACAAC
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAAACCAGACAAGGTGTGGTGGGCCAAG
AACAGCCAGGCCAAAACCATTTGCCACGGAGTCTTTGTCTGCCCTGCAGTGTGTGAAGGATATAGAATGTGTGCC
AGTTTTGATTCCCTGCCACCTTGCTGTGTGGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAA
GCAGAGCCCTGAAGACTTCAATGATGTCATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAG
CTCCCCATCAGTTTCATGGAAAATAACTCAGTGCCCTGCTGGGAACCCAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGGCAACCCCTTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGGAATGCTGATAAACCAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGGAACTGACGTTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGTGGTCTTAAAGGCTGCCAGCGCCTTGCCAAAATGGAGCTTGTA
AGAAGGCTCATGCCATTGACCCCTCTTAATTCCTCTCCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAAGACCAGAAAACAAAAGCATCAGAATTATCTTTTCCCTATGTCCAGCTT
GATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAAGTCTTTGACGGAAACCTCCAGCAATGGGCCCTCTGCTAGGG
CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCCTAACATCTCTATTCCAAACTGT
GGCGGTTTACCTGGATACCTTGGGAAGGATCCTTCCACCAGCCCCAATTACCCAAAGCCGCATCCTGAGCTGGCTTAT
TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAACTAAACTTCAAAGAGATTTTCTAGAAATAGAC
AAACAGTGCAAAATTTGATTTTCTTGCCATCTATGATGGCCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT
GGCCGTGTGACTCCACCTTCGAATCGTCATCAAACTCTCTGACTGTCTGTGTTGTCTACAGATTATGCCAATTCT
TACCGGGGATTTTCTGCTTCTTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTTCT
GACAGGATGAGAGTTATTATAAGCAAATCTTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCAACTAAAA
GACCCAACTTGCCAGACCAAATTTATCAAAATGTTGTGGAATTTTCTGTCCCCTCTAATGGATGTGGTACAATCAGA
AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACTTTTCTGTCATCCTCAACTTCTGAAGTGATCACC
CGTCAGAAACAACCTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA
GAAGATGATGTAATACAAAGTCAAAATGCACTGGGCAAATATAACACCAGCATGGCTCTTTTGAATCCAATTCA
TTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTTGAACCAAACCTTTTTTGTTCAGTTAGTCTGCAC
ACCTCAGATCCAAATTTGGTGGTGTCTTCTGATACCTGTAGAGCCTCTCCCACCTCTGACTTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTGGAGATGAACTTGTAAAGTGTATCCCTATTTGGACACTATGGGAGA
TTCCAGTTTAAATGCCTTTAAATTTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAAGTTTGTATGTGAT
AGCAGTGACCACCACTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCATATAAATGG
AAAACAGATTTCCATCATAGGACCCATTCTGTCTGAAAAGGGATCGAAGTGCAAGTGGCAATTCAGGATTTTCAGCAT
GAAACACATGCGGAAGAACTCCAAACCAGCCTTTCAACAGTGTGCATCTGTTTTCTCTCATGGTTCTAGCTCTG
AATGTGGTGAAGTGTAGCGACAATCACAGTGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTG
CAGAAGTATTAACCTAACAGGTCCAACCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAAAA

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FIGURE 344

MELVRRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTIE
RPENKSIRIIFSYVQLDPDGSCSESENIKVEDGTSSNGPLLQVCSKNDYVPVFESSSSTLTFQ
IVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQVEKD
YKIKLNFKEIFLEIDKQCKFDFLAIDGPGSTNSGLIGQVCGRVTPTFESSSNSLTVVLSTDYA
NSYRGFSASYTSIYAENINTTSLTCSSDRMRVLIISKSYLEAFNSNGNNLQLKDPTCRPKLSNV
VEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNSTVEIIYI
TEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPNLVVFLDT
CRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYLQCKVLICD
SSDHQSRCNQGCVSRSKRDISSYKWKTDSIIGPIRLKRDRSASGNSGFQHETHAEETPNQPFN
SVHLEFSEMVLAALNVVTVATITVRHFNQRADYKYQKLQNY

Important features:**Signal sequence:**

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423**Casein kinase II phosphorylation site.**amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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FIGURE 345

TGGGGGCCCCCAGGCTCGCGCGTGGAGCGAAGCAGCATGGGGCAGTCGGTGCGCGCTGGCCCTGGCGGTGCTCTC
GGCCTTGCTGTGTGTCAGGTCTGGAGCTCTGGGGTGTTCGAACTGAAGCTGCAGGAGTTCTGTCAACAAGAAGGGGCT
GCTGGGGAACCGCAATTGCTGCCGCGGGGGCGCGGGGCCACCGCCGTGCGCCTGCCGGACCTTCTTCCGCGTGTG
CCTCAAGCACTACCAGGCCAGCGTGTCCCCCGAGCCGCCCTGCACCTACGGCAGCGCCGTACCCCCGTGCTGGG
CGTCGACTCCTTCAGTCTGCCCCGACGGCGGGGGCGCCGACTCCGCGTTTACGCAACCCCATCCGCTTCCCCCTCGG
CTTCACCTGGCCGGGACCTTCTCTCTGATTATTGAAGCTCTCCACACAGATTCTCCTGATGACCTCGCAACAGA
AAACCCAGAAAGACTCATCAGCCGCCCTGGCCACCCAGAGGCACCTGACGGTGGGCGAGGAGTGGTCCCAGGACCT
GCACAGCAGCGGCCGCACGGACCTCAAGTACTCCTACCGCTTCTGTGTGACGAACACTACTACGGAGAGGGCTG
CTCCGTTTTCTGCCGTCCCCGGGACGATGCCCTTCGGCCACTTCACCTGTGGGGAGCGTGGGGAGAAAGTGTGCAA
CCCTGGCTGGAAAGGGCCCTACTGCACAGAGCCGATCTGCCCTGCCCTGGATGTGATGAGCAGCATGGATTTTGTGA
CAAACAGGGGAATGCAAGTGCAGAGTGGGCTGGCAGGGCCGGTACTGTGACGAGTGTATCCGCTATCCAGGCTG
TCTCCATGGCACCTGCCAGCAGCCCTGGCAGTGCAACTGCCAGGAAGGCTGGGGGGGCTTTTCTGCAACCAGGA
CCTGAACTACTGCACACACCATAAGCCCTGCAAGATGGAGCCACCTGCACCAACACGGGGCAGGGGAGCTACAC
TTGCTCTTGCCGGCCTGGGTACACAGGTGCCACCTGCGAGCTGGGGATTGACGAGTGTGACCCAGCCCTTGTAA
GAACGGAGGGAGCTGCACGGATCTCGAGAACAGCTACTCCTGTACCTGCCACCCGGCTTCTACGGCAAAATCTG
TGAATTGAGTGCCATGACCTGTGCGGACGGCCCTTGCTTTAACGGGGGTGGGTGCTCAGACAGCCCCGATGGAGG
GTACAGCTGCCGCTGCCCGTGGGCTACTCCGGCTTCAACTGTGAGAAGAAAATTGACTACTGCAGCTCTTCACC
CTGTTCTAATGGTGCCAAGTGTGTGGACCTCGGTGATGCCCTACCTGTGCCGCTGCCAGGCCGGCTTCTCGGGGAG
GCACTGTGACGACAACGTGGACGACTGCGCCTCCTCCCCGTGCCCAACGGGGGACCTGCCGGGATGGCGTGAA
CGACTTCTCCTGCACCTGCCCGCCTGGCTACACGGGCAGGAAGTGCAGTGGCCCGCTCAGCAGGTGCGAGCACGC
ACCTGCCACAATGGGGCCACCTGCCACGAGAGGGGCCACCGCTATGTGTGCGAGTGTGCCGAGGCTACGGGGG
TCCCAACTGCCAGTTCTTGCTCCCCGAGCTGCCCGCGGGCCAGCGGTGGTGGACCTCACTGAGAAGCTAGAGGG
CCAGGGCGGGCCATTCCTTGGGTGGCCGTGTGCGCCGGGCTCATCCTTGTCTCATGCTGCTGCTGGGCTGTGC
CGCTGTGGTGGTCTGCGTCCCGCTGAGGCTGCAGAAGCACCGGCCCCAGCCGACCCCTGCCGGGGGGAGACGGA
GACCATGAACAACCTGGCCAACTGCCAGCGTGAGAAGGACATCTCAGTCAGCATCATCGGGGCCACGCAGATCAA
GAACACCAACAAGAAGGGCGACTTCCACGGGGACCACAGCGCCGACAAGAATGGCTTCAAGGCCCGCTACCCAGC
GGTGGACTATAACCTCGTGCAGGACCTCAAGGGTGACGACACCGCCGTGAGGACCGGCACAGCAAGCGTGACAC
CAAGTGCCAGCCCCAGGGCTCCTCAGGGGAGGAGAAGGGGACCCCGACCACACTCAGGGGTGGAGAAGCATCTGA
AAGAAAAAGGCCGGACTCGGGCTGTTCAACTTCAAAAGACACCAAGTACCAGTCCGTGTACGTATATCCGAGGA
GAAGGATGAGTGGTGCATAGCAACTGAGGTGTAAAAATGGAAGTGAGATGGCAAGACTCCCGTTTCTCTTAAATA
AGTAAAATTCCAAGGATATATGCCCCAACGAATGCTGCTGAAGAGGAGGGAGGGCCTCGTGGACTGCTGCTGAGAA
ACCGAGTTCAGACCGAGCAGGTTCTCCTCCTGAGGTCTCGACGCCTGCCGACAGCCTGTGCGGGCCCGGCCGCC
TGCGGCACTGCCCTTCCGTGACGTGCGCGTTGCACTATGGACAGTTGCTCTTAAGAGAATATATATTTAAATGGGT
GAACTGAATTACGCATAAGAAGCATGCACTGCCCTGAGTGTATATTTTGGATTCTTATGAGCCAGTCTTTCTTGA
ATTAGAAACACAAACACTGCCCTTTATTTGTCCTTTTGTATACGAAGATGTGCTTTTCTAGATGGAAAAGATGTGT
GTTATTTTGGATTGTGTAATAATATTTTTCATGATATCTGTAAAGCTTGAGTATTTTGTGATGTTCTGTTTTTA
TAATTTAAATTTTGGTAAATATGTACAAAGGCACCTTCGGGTCTATGTGACTATATTTTTTGTATATAAATGTAT
TTATGGAATATTGTGCAAATGTTATTTGAGTTTTTTTACGTGTTTTGTTAATGAAGAAATTCCTTTTTAAATATTT
TTCCAAAATAAATTTTATGAATGACAAAAA
AAAAAA

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FIGURE 346

MGSRCALALAVLSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGAGPPPCACRTFFRVC
LKHYQASVSPEPPCTYGS AVTPVLGVDSFSLPDGGGADSAFSPNPIRFPFGFTWPGTFSLIIEA
LHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKYSYRFVCDEHYGEGCS
VFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVGWQGR
YCDECIRYPGCLHGTCQQPWOCNCQEGWGGLFCNQDLNYCTHHKPKNGATCTNTGQGSYTCS
CRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCTCPPGFYGKICELSAMTCADGPCFNG
GRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQAGFSGRHCD
DNVDDCASSPCANGGTCRDGVNDFSCCTPPGYTGRNCSAPVSRCEHAPCHNGATCHERGHRYV
CECARGYGGPNCQFLLPELPPGPAVVDLTKLEGQGGFFPWVAVCAGVILVLMMLLLGCAAVVV
CVRLRLQKHRPPADPCRGETETMNNLANCQREKDISVSIIGATQIKNTNKKADFGDHSADKN
GFKARYPAVDYNLVQDLKGDDTAVRDAHRSKRDTCQPOGSSGEEKGTPTTLRGGEASERKRPD
SGCSTSKDTKYQSVYVISEEKDECVIATEV

Important features:**Signal sequence:**

Amino acids 1-21

Transmembrane domain:

Amino acids 546-566

N-glycosylation site:

Amino acids 477-481

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 660-664

Tyrosine kinase phosphorylation sites:

Amino acids 176-185;252-261

N-myristoylation sites:Amino acids 2-8;37-43;40-46;98-104;99-105;262-268;281-287;
282-288;301-307;310-316;328-334;340-344;378-384;387-393;512-518;
676-682;683-689;695-701**Aspartic acid and asparagine hydroxylation sites:**

Amino acids 343-355;420-432;458-470

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 552-563

EGF-like domain cysteine pattern signature:Amino acids 243-255;274-286;314-326;352-364;391-403;429-441;
467-479;505-517

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FIGURE 347

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAACA
TCGTAGTCCACCCCCTCCCCATCCCCAGCCCCGGGGATTGAGGCTCGCCAGCGCCCAGCCAG
GGAGCCGGCCGGGAAGCGCG**ATG**GGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGCTGT
TCGCCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGGACAT
CTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGGCTCAAGTGCCAAGTGAAAGATCACGAGG
ACTCATCCCTGCAATGGTCTAACCCCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGAGAGCCC
TTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGCATCAGCA
ATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGTGCGAACTG
CCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTTATAAATCTT
CATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTTCTGGGAGCAAGCCTGCAGCCC
GGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCATACAGGAAGATC
CCAATGGTAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCCGGGAGGATGATG
GGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGACAGATCCACCTCTC
AACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCCTCCCCATCCTCGTG
AGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCCCCCAGCAGTACCTAT
GGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGTGCCCTGATCTTCCCTT
TCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAGCAACATGGGCAGCTACA
AGGCCTACTACACCCTCAATGTTAATGACCCCAGTCCGGTGCCCTCCTCCTCCAGCACCTACC
ACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCCTGCTGCTCATCATGCTCATCTTCC
TTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACATGAGGCAAAAGGCTCCGACG
ATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCGGGCAGTCAGGAGGGGACGACA
AGAAGGAATATTTTCATC**TAG**AGGCGCCTGCCCCTTCTGCGCCCCCAGGGGGCCCTGTGGGG
ACTGCTGGGGCCGTCACCAACCCGGACTTGTACAGAGCAACCGCAGGGCCGCCCCCTCCCGCTT
GCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGCTTTGGGTGCGGTTTTGTACTCGGT
TTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGGAGGGTTGCCCTCAGCCCTTTCCGTGGCTT
CTCTGCATTTGGGTTATTATTATTTTTGTAACAATCCCAAATCAAATCTGTCCTCAGGCTGGA
GAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACAAACAAAAACA

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FIGURE 348

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQWS
NPAQQTLYFGEKRALRDNRIQLVTSTPHELSSISINVALADEGEYTCSTFTMPVRTAKSLVTV
LGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFT
VSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQKLLL
HCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLN
VNDPSPVPSSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDDAPDADT
AIINAEGGQSGGDDKKEYFI

Important features:**Signal sequence:**

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

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FIGURE 349

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAGGACAGCAGCAAAG
AGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTACCATACGCCCTCAGGACGTTCCCTCTA
GCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGTCATTTTGATTTTGCTGTTTATTTTTTTTTTCTTTTCTT
TTTCCCACCACATTGTATTTTATTTCCGTACTTCAGAAATGGGGCTACAGACCACAAAGTGGCCCAGCCATGGGG
CTTTTTTTCCTGAAGTCTTGGCTTATCATTTCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCCCTA
GTGTGTGCCGCTGCGACAGGAAGTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTGCCTCTTGGGATCCCGG
AGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGCTGGATTTCTGCAGAACTGCACAATGTAC
AGTCGGTGCACACGGTCTACCTGTATGGCAACCAACTGGACGAATTCCTCATGAACCTTCCCAAGAATGTCAGAG
TTCTCCATTTGCAGGAAAAACAATATTCAGACCATTTCACGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGC
TGCACCTGGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGCTATTAGCCTCAAAT
TGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCCTGTGGACTTGCAAGAGCTGAGAGTGG
ATGAAAATCGAATTGCTGTATATCCGACATGGCCTTCCAGAATCTCACGAGCTTGGAGCGTCTTATTGTGGACG
GGAACCTCCTGACCAACAAGGCTATCGCCGAGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTG
TACGTAATTGCTGTCCCACCTTCCTCCCGATCTCCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACC
AGATAAACCACATTCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCAACAACCAAC
TGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTCACTGCTCGGAATAACCCCTTGGT
TTTGTGACTGCAGTATTAAATGGGTACAGAAATGGGTCAAATATATCCCTTCATCTCTCAACGTGCGGGGTTTCA
TGTGCCAAGGTCTGAAACAAGTCCGGGGGATGGCCGTGAGGGAATTAAATATGAATCTTTTGTCTGTCCCACCA
CGACCCCCGGCCTGCCTCTCTTCACCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCTCTCTA
TTCCAAACCTTAGCAGAAGCTACACGCTCCAACTCCTACCACATCGAACTTCCCACGATTCTGACTGGGATG
GCAGAGAAAGAGTGACCCCACTTATTTCTGAACGGATCCAGCTCTCTATCCATTTTGTGAATGATACTTCCATTC
AAGTCAGCTGGCTCTCTCTCTTCAACCGTGATGGCATACAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAG
GGGGCATCGTTTCAAGGAGCGCATAGTCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCA
CCTATCGGATTTGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAAGGCCA
CCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGACGTCCACAGCATGG
GCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTTGTGCTGGTGGTCTTGTCTCAGCGTCTTTT
GCTGGCATATGCACAAAAGGGGCGCTACACCTCCCAGAAGTGGAAATACAACCGGGGCGGGCGGAAAGATGATT
ATTGCGAGGCAGGCACCAAGAAGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTTTCAGATCGTCTCCTTAA
ATAACGATCAACTCCTTAAAGGAGATTTAGACTGCAGCCCATTACACCCCAAATGGGGGCATTAAATTACACAG
ACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGCACTGCCATACGTTGACAGC
CAGAGGCCACAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAACACACTCGTGTGTGCACATAAAGACACGCAG
ATTACATTTGATAAATGTTACACAGATGCATTTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAA
TGGGATTTAAAAAAGTGCTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACTCTTTGCTTTTTAA
TCTT

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FIGURE 350

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIPE
GVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFFMNLPKNVRVLHLQENNIQTISR
AALAQLLKLEELHLDNDSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELRVDE
NRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPDLPGT
HLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNNPWFCD
CSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMVRELNMMNLLSCPTTTPGLPLFTPAPSTAS
PTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISERIQLSIHFVNDTSIQVSW
LSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPLDAFNRYAV
EDTICSEATTHAŞYLNNGSNTASSHEQTTSMSGSPFLLAGLIGGAVIFVLVLLSVFCWHMH
KKGRTYSQKWYNRGRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKGD FRLQPIYTP
NGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Important features:**Signal peptide:**

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639**Amidation site.**

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

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FIGURE 351

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGACGTTGGCAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA
TGAAAGGGCTTCECCGCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCGCGAGGGAGGAGCGCGCACCGGACCGC
GAGGGCGGGCGTGCACCTCGGCTGGAACTTTGTGCCGGGGCCCCGAGCGCGCGCGGGCTGGGAGCTTCGGGTAGA
GACCTAGGCGCGCTGGACCGCGATGAGCGCGCGGAGCCTCCGTGCGCGCGCGCGGGGTTGGGGCTGCTGCTGTGC
GCGGTGCTGGGGCGCGCTGCGCGGTCCGACAGCGGCGGTGCGCGGGGAACCTCGGGCAGCCCTCTGGGGTAGCCGCC
GAGCGCCCATGCCCACTACCTGCCGCTGCCCTCGGGGACCTGCTGGACTGCAGTCGTAAGCGGCTAGCGCGTCTT
CCCGAGCCACTCCCGTCTCGGTGCTCGGCTGGACTTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCC
ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACAAATGAATTGGAGACCATTCCAAATCTGGGACCA
GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAACTGCATTTCCAGCCCTACAG
CTCAAATATCTGTATCTCAACAGCAACCCGAGTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACA
CTCCTTGTGTTAAAGCTGAACAGGAACCCGAATCTCAGCTATCCACCCAGATGTTTAAACTGCCCCAACTGCAA
CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGGTGTCTGAAGTCT
CTGAAAATGCAAAGAAATGGACTAACGAACTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAAATTTTG
CAGCTGGACCATAACAACCTAACAGAGATTACCAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCAT
CTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATACACTGCACATTTGG
AACAACAGAGTCAGCTACATTGCTGATTGTGCTTCCGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAAC
AATGAAATTTCTGGACTATTGAAGACATGAATGCTGCTTCTCTGGCTTGACAACTGAGGCGACTGATACTC
CAAGGAAATCGGATCGTTCTATTACTAAAAAAGCCTTCACCTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATTGCATTTAAATACA
TCAAGCCTTTTGTGCGATTGCCAGCTAAAAFGGCTCCACAGTGGGTGGCGGAAAACAACCTTTAGAGCTTTGTA
AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAGGAAGAAGCATTTTGTGCTGTTAGCCAGATGGCTTTGTGTGT
GATGATTTTCCCAAACCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCTCAATGACTTTTGCCTTGGAAAAAGACAATGAACACTACTGCATGAT
GCTGAAATGGAAATTTATGCACACCTCCGGGGCCAAAGTGGCGAGGTGATGGAGTATACCACCATCCTTCGGCTG
CGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCTCCAATCACTTTGGTTCATCTACTCTGTG
AAAGCCAAGCTTACAGTAAATATGCTTCCTCATTACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC
ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGGCACAGAC
TTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCGAGGATGACGTGTTCTTTATCTGGATGTGAAGATA
GAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTAGCAATGCAACTCTGACTGTC
CTAGAAACACCATCATTTTTTGGGGCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAACTGAACTGGACCAAGATGATAGCCCATTTGGTGGTAACCGAGAGGCAC
TTTTTTGCAGCAGGCAATCAGCTTCTGATTATTTGTGGACTCAGATGTGATGCTGGGAAATACACATGTGAG
ATGCTAACACCCCTTGGCACTGAGAGAGGAAACCTGCGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCT
CAGATGACAGCCCCATCGTTAGACGATGACGGATGSGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGTGT
GTGGTGGGCACGTCACTCGTGTGGGTGGTTCATCATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACC
AACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTATCTCAGGGAACGTTAGCTGACAGGCAG
GATGGGTACGTGTCTTCAGAAAGTGAAGCCACCACAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCA
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTT
CTTTGTCCGTTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGATCCTTTTGAACA
TATCATACAGGTTGCAGTCTGACCCAAGAACAGTTTAAATGGACCCTATGAGCCAGTTACATAAAGAAAAAG
GAGTGCTACCCATGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACAT
GTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC
TCTTTAGATTTTAGTGCAAAATCCAGAGCCAGCGTCCGTTGCCCTCAGTAATTCCTTCATGGGTACCTTTGGAAAA
GCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTGAGCCAAGAGCCTTTTAT
TTGAAAGCTCATTCTTCCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAA
GAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAGGAAAGCTTAACATATCTACCTCAAGTGAACCTTTTATTTAAAGAGAGAGAAT
CTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGCTTTATTTATACAGATGAACCAAAATAC
AAAAAGTTATGAAAATTTTATCTGGGAATGATGCTCATATAAAGAAATACCTTTTTAACTATTTTTAACTTTG
TTTTATGCAAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGA
TTTCTTTTTATGAAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTTTTAAATAGAAGTT
ACTTCATTATATTTTGCACATTATATTTTAAATAAATGTGTCAATTTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 352

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLLDCSRKRLARLPEPLPSW
 VARLDLSHNRSLFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANITLLSLAGNRIVEILPEHLKEFQSLETL
 DLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEPGYFDNLANTLLVLKLNRRNISAIPPKMFKLPQLQHLELNRN
 KIKNVGDLTFQGLGALKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIN
 RISPDWAEFCQKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSSLKTLDLKNNEISWTI
 EDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSOMKKLQQLHLNTSSLLCDC
 QLKWLFPQWVAENNEQSFVNASCAPQLLKGRSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASS
 SDSPMTFAWKKNELLHDAEMENYAHLEAQQGEVMEYTTILRLREVEFASEGKYQCVISNHFSSYSVKAKLTVN
 MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDGTDFFAARERRMHVMPEDDVFVIVDKIEDIGVYS
 CTAQNSAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDSPLVVTERHFFAAGNQ
 LLIIIVSDSDVSDAGKYTCEMSNTLGTGERGNVRLSVIPTCTCDSPQMTAPSLDDDGWATVGVVIAVCCVVGTSLV
 WVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTLADRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGT
 CHIDNSSEADVEAATDLFLCPFLGSTGPMYLGKNVYGSDFETYHTGCSPPRTVLMQHYEPSYIKKKECYPCSH
 PSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDPSANPEFASVASSNSFMGTFGKALRRPHL
 DAYSSFGQPSDCQPRAFYLKAHSSPDLDSGSEEDGKERTDFQENNHICTFKQTLNRYRTPNFQSYDLDT

Important features:**Signal sequence:**

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

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FIGURE 353

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTTCTTCTCCTTTCTGGCTTCGGACATTGG
AGCACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTGTACTTTGTGATGAGATCGGGGATGA
ATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTTGCTGGAGACGCTCTCTTTGTTTTGCCGCTGGAAACGTTAC
AGGGGACGTTTGC AAAGAGAAGATCTGTTCCCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAA
GGGCTTCACAAGTCTGCAGCGTTTCACTGCCCGGACTTCCCAGTTTACCATTATTTCTGCATGGCAATTCCCT
CACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGGAAAACAATGGCTTGCA
TGAAATCGTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGGCTGCACATCAACAACAACAAGATCAAGTC
TTTTCGAAAGCAGACTTTTCTGGGGCTGGACGATCTGGAATATCTCCAGGCTGATTTAATTTATTACGAGATAT
AGACCCGGGGGCTTCCAGGACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCCCTACC
TGCCAACGTGTTCCAGTATGTGCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCCCTATGA
GGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCCTGGGACTGCACCTGTGATCT
GCTCTCCCTGAAAGAATGGCTGGAAAACATTCCCAAGAATGCCCTGATCGGCCGAGTGGTCTGCGAAGCCCCCAC
CAGACTGCAGGGTAAAGACCTCAATGAAACCACCGAACAGGACTTGTGTCTTTGAAAACCGAGTGGATTCTAG
TCTCCCGGGCCCCCTGCCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCA
AGAGGATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGATCAAAATCAG
ACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCCTTAGCTAACAGTTTACCCTGCCCTGGGGGCTG
CAGCTGCGACCACATCCCAGGGTGGGTTTAAAGATGAACTGCAACAACAGGAACGTGAGCAGCTTGGCTGATTT
GAAGCCCAAGCTCTCTAACGTGCAGGAGCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAATCGCACTT
TGTGGATTACAAGAACCTCATTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAA
GAACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGAGAAATTCGCGGG
GCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCATCCTCCCGGGCACTTTCAATGCCAT
GCCCAAACCTGAGGATCCTCATTCTCAACAACAACCTGCTGAGGTCCCTGCCCTGTGGACGTGTTGCTGGGGTCTC
GCTCTCTAAACTCAGCCTGCACAACAATTACTTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTC
CATCATCCAGATAGACCTCCACGGAAACCCCTGGGAGTGTCTCTGCACAATTGTGCCTTTCAAGCAGTGGGCAGA
ACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTCTTTAGAAAGGATTTTAT
GCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCTCGCCACGTTAACTTCGCACAGTAAAAA
CAGCACTGGGTTGGCGGAGACCGGGACGCACTCCAACCTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTT
GGTCCCGGGACTGCTGCTGGTGTGTTGTACCTCCGCCTTACCCTGGTGGGCATGCTCGTGTATCTGAGGAA
CCGAAAGCGGTCCAAGAGACGAGATGCCAACTCCTCCGCTCCGAGATTAAATCCCTACAGACAGTCTGTGACTC
TTCCTACTGGCACAATGGGCCTTACAACGAGATGGGGCCCCACAGAGTGTATGACTGTGGCTCTCACTCGCTCTC
AGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCGATACATCCTTCCCCACCGCAGGCACCCCGG
GGCTGGAGGGGCGTGTACCCAAATCCCCGCGCCATCAGCCTGGATGGGCATAAGTAGATAAATACTGTGAGCTC
GCACAACCGAAAGGGCCTGACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGA
GCGCAGCCAGCTCGCTCTTTGCTGAGAGCCCCCTTTTGACAGAAAGCCAGCACGACCCCTGCTGGAAGAACTGACA
GTGCCCTCGCCCTCGGCCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATACATATATACATATATCCACATC
TATATAGAGAGATAGATATCTATTTTTTCCCTGTGGATTAGCCCCGTGATGGCTCCCTGTTGGCTACGCAGGGAT
GGGCAGTTGCACGAAGGCATGAATGTATTGTAAATAAGTAACTTTGACTTCTGAC

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FIGURE 354

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYHL
FLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQTF
LGLDDLEYLQADFNLLRDIDFGAFQDLNKLEVLIILNDNLISTLPANVFQYVPITHLDLRGNRL
KTLPYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ GKDL
NETTEQDLCP LKNRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTKIPGNW
QIKIRPTAAIATGSSRNKPLANS LPCPGGCSCDHIPGSG LKMNCNNRNVS SLADLKPKLSNVQ
ELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNYLDTLSRE
KFAGLQNLLEYLNVEYNAIQ LILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSLSKLSLHNN
YFMYLPVAGVLDQLTSIIQIDLHGPNWECSC TIVPFKQWAERLGSEVLMSDLKCETPVNFFRK
DFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVLVPGLLLVFVT
SAFTTVVGMLVFILNRNRKRSKRRDANSSASEINSLQTVCDSSYWHNGPYNADGAHRVYDCGSHS
LSD

Important features:**Signal sequence:**

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697**N-myristoylation site.**amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

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FIGURE 355

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCCTGACCCCAGAATAACTCAGGGCTGCACCGGGCCTG
GCAGCGCTCCGCACACATTTCTTGTGCGGGCCTAAGGGAAACTGTTGGCCGCTGGGCCCCGGGGGGGATTCTTGG
CAGTTGGGGGGTCCGTCCGGAGCGAGGGCGGAGGGGAAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAG
GGCGGTGACCGCGCTCCAGACACAGCTCTGCGTCCCTCAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGC
GGGGCCTCAGAGAATGAGGGCCGGCGTTCCGCCCTGTGCCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCCGGCGCGG
CGAACACCCCCACTGCCGACCGTGCTGGCTGCTCGGCCCTCGGGGGCCTGCTACAGCCTGCACCACGCTACCATGAA
GCGGCAGGCGGGCCGAGGAGGCCCTGCATCCTGCGAGGTGGGGCGCTCAGCACCGTGCGTGCGGGCGCGGAGCTGCG
CGCTGTGCTCGCGCTCCTGCGGGCAGGCCCGAGGGCCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACT
GGAGCGCAGGCGTTCCCACTGCACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCCG
CGGTCTCGAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGCGGTACT
CCAGGCCACCGGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGCGCGCCAACGGCTACCTGTG
CAAGTACCAGTTTGAGGTCTTGTGTCTTGTGCGCGCGCCCCGGGGCCGCTCTAACTTGAGCTATCGCGCGCCCTT
CCAGCTGCACAGCGCCGCTCTGGACTTCAGTCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGGACAGCTCCC
GATCTCAGTTACTTGCATCGCGGACGAAATCGGCGCTCGCTGGGACAAACTCTCGGGCGATGTGTTGTGTCCCTG
CCCCGGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGGCTTTGCCCTG
CGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGSCCGCTCTTGTGTGACCAGTGGGGAAGGACAGCCGACCCT
TGGGGGGACCGGGGTGCCCCACCAGGCGCCCCGCGGCCACTGCAACCAGCCCCGTGCCGCAGAGAACATGGCCAAT
CAGGGTCGACGAGAAGCTGGGAGAGACACCACTTGTCCTGAACAAGACAATTTCAGTAACATCTATTCTCTGAGAT
TCCTCGATGGGGATCACAGAGCACGATGTCTACCCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCAC
CCCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTTCGACTCCTCCTC
TGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTTGGTGATCTTGACCATGACAGTACTGGGGCTTGT
CAAGCTCTGCTTTCACGAAAGCCCCCTCTTCCCAGCCAAGGAAGGAGTCTATGGGCCCCGGGGCCTGGAGAGTGA
TCCTGAGCCCCGCTGCTTTGGGCTCCAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCT
GCGGGACAGAGCAGAGGGTGCCCTTGCTGGCGGAGTCCCCCTCTTGGCTCTAGTGATGCATAGGGGAAACAGGGGACA
TGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGGAACCAAGAGGAACTTACTTGTGTAAGTACAA
TTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCACTGAGGAGCTAAATCAGAACTGCACACTCCTTC
CCTGATGATAGAGGAAGTGGAAGTGCCCTTTAGGATGGTGATCTGGGGGACCGGGTAGTGCTGGGGAGAGATATT
TTCTTATGTTTATTTCGAGAATTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATAT
AATTTACATTAAAAATAATTTCTACCAAATGGAAAGGAAATGTTCTATGTTGTTCAGGCTAGGAGTATATTGG
TTCGAAATCCAGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

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FIGURE 356

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALST
VRAGAE LRAVLALLRAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLESD
TLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGAASN
LSYRAPFQLHSAALDFSPFGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPGRYLR
AGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATATSPVP
QRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITPSGSVIS
KENSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMTVLGLVKLCFHESPSSQPRKESMGPP
GLES DPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Important features:**Signal sequence:**

amino acids 1-16.

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

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FIGURE 357

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCATTTTGGGAAGA
AGACTAAAAATGGTGTGTTTCCAATGTGGACACTGAAGAGACAAATTCTTATCCTTTTAAACATAATCCTAATTTCC
AAACTCCTTGGGGCTAGATGGTTTCTAAAACCTCTGCCCTGTGATGTCACCTCTGGATGTTCCAAAGAACCATGTG
ATCGTGGACTGCACAGACAAGCATTGACAGAAATTCCTGGAGGTATTCCCACGAACACCACGAACCTCACCCCTC
ACCATTAACCACATACCAGACATCTCCCCAGCGTCTTTCACAGACTGGACCATCTGGTAGAGATCGATTTCAGA
TGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAGC
TTTAGTGGACTCACTTATTTAAATCCCTTTACCTGGATGGAAACCAGCTACTAGAGATACCGCAGGGCCTCCCG
CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACACATCTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC
AACATAGAAATACTCTACCTGGGCCAAAACCTGTTATTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAA
GATGCCTTCCATAAATTTGACAAAGTTAAAAGTGCTCPCCTGAAAGATAACAAATGTCACAGCCGTCCTTACTGTT
TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATGATTTTAATAAC
CTCAACCAATTACAAATTTCTTGACCTAAGTGGAAATTGCCCTCGTTGTTATAATGCCCCATTTCTTGTGCGCCG
TGTAATAATAATTCTCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGACAGAATTAAGTGTTCACGTCTA
CACAGTAACCTCTCTTACAGCATGTGCCCCAAGATGGTTAAGAACATCAACAACTCCAGGAACCTGGATCTGTCC
CAAACTTCTTGGCCAAAGAAATTGGGGATGCTAAATTTCTGCATTTCTCTCCCCAGCCTCATCCAATTGGATCTG
TCTTTCAATTTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCACAAGCATTTTCTTCACTGAAAAGCCTG
AAAATTTCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA
AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAGA
CTGAAAGTCATAGATCTTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAAT
GCCAGAACTTCTGTAGAAAGTTATGAACCCAGGTCTTGGAAACAATTACATTATTTTCAGATATGATAAGTATGCA
AGGAGTTGCAGATTCAAAAACAAGAGGCTTCTTTTCATGTCTGTTAATGAAGCTGCTACAGTATGGGCAGACC
TTGGATCTAAGTAAAAATAGTATATTTTTTGTCAAGTCTCTGATTTTCAGCATCTTTCTTTCTCAATGCCTG
AATCTGTCAAGAAATCTCATTAGCCAAACTCTTAATGGCAGTGAATTCCAACCTTAGCAGAGCTGAGATATTTG
GACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCACAACTGGAAGTTCTGGAT
ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAAACTTTACCAAGAACCTAAAGGTT
CTGCAGAACTGATGATGAACGACAATGACATCTCTCCTCCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA
ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAG
AATCTGCTAAAATTAGAGGAATTAGACATCTCTAAAAATTCCTAAGTTTCTTGCCTTCTGGAGTTTTTGTATGGT
ATGCCTCCAAATCTAAAGAATCTCTTTGGCCAAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCCAGTGT
CTAAAGAACCTGGAACTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAGAGATTATCCAAGTGTTC
AGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTCTACAAGATGCCTTC
CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAGACCAGCTTCCAGAAAATGTCTC
AACAACTCTGAAGATGTTGCTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGG
GTTAACCATACGGAGGTGACTATTCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC
CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA
TCTGTATCTCTCTTTCTCATGGTGATGATGACAGCAAGTCACTCTATTTCTGGGATGTGTGGTATATTTACCAT
TTCTGTAAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTAT
GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAGAGAGAAA
CATTTTAAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTTCCAGAGCATA
CAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAGACTGAAAATTTTAAAGATAGCATTTTAC
TTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTCAGAAG
TCCAAGTTCTCCAGCTCCGGAAAAGGCTCTGTGGGAGTTCTGTCTTGAAGTGGCCAAACACCCGCAAGCTCAC
CCATACTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCTATAGTCAGGTGTTCAAGGAA
ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCTGGC

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FIGURE 358

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGGI
PTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRCNCVPIPLGSKNNMCIKRLQIKPRSFSGL
TYLKSLYLDGNQLEIIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLQNCYYRNPC
YVSYSIEKDAFLNLTCLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNLNQLQ
ILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWFKNINK
LQELDLSQNF LAKEIGDAKFLHFLPSLIQLDLSFNFELOVYRASMNLSQAFSSLKSLKILRIR
GYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKISPSGDSSE
VGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQTLDSLKNS
IFFVKSSDFQHLSEFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRDLHLHSTAFEELHK
LEVLDISSNSHYFQSEGITHMLNFTKNLKVQLQKMMNDNDISSSTSRTMESESLRTLEFRGNH
LDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSLAKNGLKSFSWK
KLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQDAFQLRYLDLSS
NKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDAVWFVWVNHTEVTIIPYLATDVTVCVGPGA
HKGQSVISLDLYTCELDLTNLILFSLISISVSLFLMVMMTASHLYFWDVWYIYHFCKAKIKGYQ
RLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLEERDWLPGQPVLENLSQ
SIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLEKPFQKSKFLQLRKRLC
GSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

Important features:**Signal sequence:**

amino acids 1-26

Transmembrane domain:

amino acids 840-860

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FIGURE 359

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTAC
TGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGTGG
AGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGAGAT
GGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCACAACA
AGGAGCGCGGGCGCCGCGGCGAGAATCTGTTCGCCATCACAGACGAGGGCATGGACGTGCCGC
TGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCTGCAGCC
CAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATCGGCTGTG
GTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACTGGTGTGCA
ACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTCCGTGCTCCC
AATGTCCCTCTGGCTACCACTGCAAGAATCCCTCTGTGAACCCATCGGAAGCCCGGAAGATG
CTCAGGATTTGCCTTACCTGGTAACTGAGGCCCCATCCTTCCGGGCGACTGAAGCATCAGACT
CTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCTTGGTAACAGAGG
TCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCCCCAACTTCCTTAG
CAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAACAACCTGAGGTCCCTT
CCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTACCTTCCCCAAATCGA
CCCATGTTCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACAAAAGTGCCCTCTAGGA
GCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAGGGAACCTACCCCATG
CCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTGAGGTCTTGGCCTCAGTTT
TTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGACCACACGGGGCACACCTCCT
CCAAGTCCCTGCCCAATTTCCCCAATACTCTGCCACCGCTAATGCCACGGGTGGGCGTGCCC
TGGCTCTGCAGTCGTCTTGGCAGGTGCAGAGGGCCCTGACAAGCCTAGCGTTGTGTCAGGGC
TGAATCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGACTACTGCTCCTGCCTCCTCTGG
TGTTGGCTGGAATCTTCTGAATGGGATACCACTCAAAGGGTGAAGAGGTCAGCTGTCCTCCTG
TCATCTTCCCCACCCTGTCCCCAGCCCCTAAACAAGATACTTCTTGGTTAAGGCCCTCCGGAA
GGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCCATCCTGGAGGCACAAGGCCTGGCTG
GCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACCGGGCCACACCTCTCCTGCCCTCCC
TCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCTCACTGCCTACCTGGCCTGGGGCTGTCT
GCCCACACAGCATGTGCGCTCTCCCTGAGTGCCTGTGTAGCTGGGGATGGGGATTCTAGGGG
CAGATGAAGGACAAGCCCCACTGGAGTGGGGTTCTTTGAGTGGGGAGGCAGGGACGAGGGAA
GGAAAGTAACTCCTGACTCTCCAATAAAAACCTGTCCAACCTGTGAAA

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FIGURE 360

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEEL
AAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQMC
GHYTQVWAKTERIGCGSHFCEKLGQVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCPSG
YHCKNSLCEPIGSPEDAQDLPLYLVTEAPSRATEASDSRKMGTTPSSLATGIPAFLVTEVSGSL
ATKALPAVETQAPTSLATKDPSPMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKSTHVPI
PKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEAEELPPSSEVLASVFPAQD
KPGELQATLDHTGHTSSKSLPNFPNTSATA¹NATGGRALALQSSLPGAEGPDKPSVVSGLN²SGP
GHVWGPELLGLLLLPLVL³AGIF

Important features:

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

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FIGURE 361

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTGG
GGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAAGCGCGGGGGCTGGAGCACCACCAACT
GGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACTGCG
AGAGGACCCCGGCGTCCGGGCTCCCGGTGCCAGCGCT**ATG**AGGCCACTCCTCGTCCTGCTGCT
CCTGGGCCTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGCCCCGGG
GCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGCCGCGATGG
CCGCGACGGCCGCGACGGCGCGCCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGAGGCCGGG
ACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGGGCCACCGG
GCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCC**TTC**AGCGCCAAGCGCTCCGAGAGCCG
GGTGCCCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACGAGCAGGGACA
TTACGACGCCGTCACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTACTTCGCCGTCCA
TGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGAATCCATTGCCTC
TTTCTTCCAGTTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGGGGGCCATGGTGAG
GCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGC
CAGCATCAAGACAGACAGCACCTTCTCCGGATTTCTGGTGTACTCCGACTGGCACAGCTCCCC
AGTCTTTGCT**TAG**TGCCCCACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGTGA
GGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCCTGGAATATTGTGAATGACTAGGGAGG
TGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATGGGAACAGTGGCTGTCTGCGATCA
GGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCAGAGGAGTGTGCTGTGCTGG
CAAGTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGTGGGGTGCTCTCTTCCTGGTC
CTCTGCTTCTCTGGATCCTCCCCACCCCTCCTGCTCCTGGGGCCGGCCCTTTTCTCAGAGAT
CACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 362

MRPLLVLALLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPG
EKGEGRPGRLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFD
RVLVNEQGHYDAVTGKFTCQVPGVYFVAVHATVYRASLQFDLVKNGESIASFFQFFGGWPKPA
SLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

Important features:**Signal sequence.**

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

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FIGURE 363

[illegible]

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FIGURE 364

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLS DAPHDDAHGNFQYDHEAFLGRE
VAKEFDQLTPEESQARLGRIVD RMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDTYD
TDRDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATREELT
AFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQFRDF
RDLNKDGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFVGSQAT
NYGEDLTRHHDEL

Important features:**Signal sequence:**

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302**N-myristoylation site.**

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

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FIGURE 365

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCG**ATG**GGGACAAAG
GCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGGCA
TTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCTGTG
AAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCAAGGA
GACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGGTGACC
TTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATACACTTGT
ATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGTGCTTGTG
CCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGGGCAGTGCTG
ACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGATGGGATAGTG
ATGCCTACGAATCCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCTGAATCCCACA
ACAGGAGAGCTGGTCTTTGATCCCCGTGACGCTCTGATACTGGAGAATACAGCTGTGAGGCA
CGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAAT
GTGGGGGTCATCGTGGCAGCCGTCTTGTAAACCCTGATTCTCCTGGGAATCTTGTTTTTGGC
ATCTGGTTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGACTTCGAGTAAGAAG
GTGATTTACAGCCAGCCTAGTGCCCCGAAGTGAAGGAGAATTCAAACAGACCTCGTCATTCCCTG
GTG**TGA**GCCTGGTTCGGCTCACCGCCTATCATCTGCATTTGCCTTACTCAGGTGCTACCGGACT
CTGGCCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTCTACACCCACAGGGCCC
CCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCCATCCTCCTTCATGCCCTC
CCTCCCTTTCCCTACCACTGCTGAGTGGCCTGGAACCTTGTTTAAAGTGTTTATTCCCCATTTCT
TTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCCTTCTAAGTAGACAGCAAAAA
TGGCGGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGCTGGCAGGGATCTTTGAATAGG
TATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGACGACCAGGGCCAGCTGTTCTAGA
GCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGGTGATGACACTGGGGTCCTTCCAT
CTCTGGGGGCCACTCTCTTCTGTCTTCCCATGGGAAGTGCCACTGGGATCCCTCTGCCCTGTC
CTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGTGGAAAATGGGAGCTCTTGTTGTGGA
GAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAGGATTTAAAACCGCTGCTCTAAAGAAA
AGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTGTAATCCCAGAGGCTGAGGCAGGCGGAT
CACCTGAGGTGCGGAGTTCGGGATCAGCCTGACCAACATGGAGAAACCCTACTGGAAATACAA
AGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTCCCAGCTGCTCAGGAGCCTGGCAACAAGAG
CAAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

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FIGURE 366

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEWK
FDQGDTRRLVCYNNKITASYEDRVTEFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKVKL
IVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYV
LNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVTLLILLGI
LVFGIWFAYSRRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Important features:**Signal sequence:**

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

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FIGURE 367

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAATG
AAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTTAGACCCGCGGGGGTGGTGTGTTCTGACATAAAATAAATAATCTTAAAGCAGCTGTTCCCCTCC
CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTACACAAAGAAAAAGTATGTTCATTTTCTC
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTTGGAAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAAAGAAC
GGTGTGGTGGTGTGTTTCTTTTCTTTTGAATTTCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
TTTGTGCCATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTTTTTTTAAAT
TTTTATTCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAAACCACCTGGATTTCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACCTGTTTGAATTCAGAAGGACCAACACCAGATAAAATTAAGAATCTGAAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAAACAGGGCCCTATTTGACCCCTGCTTGTGGTGTGCT
GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA
CCAGTTTCAGCAAGGTGATTTGTGTTCCGGAAGAACCTGCGTGAGGTTCGGGATGGCATCTCCACCAACACACGGCT
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCATTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTCAATGGTCTGGCGAACCTCAACACTCTGGA
ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATCTTGTCTAAACTGAAGGAGCTCTGGTT
GCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCTTCTTTGCGCCGACTAGACTTAGG
GGAATTGAAAAGACTTTTATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACCTGAGGTATTTGAACCTTGC
CATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTTTCTGGGAATCA
TTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTTGTATGCACCTTCAAAAACCTGTGGATGATACAGTCCCAGAT
TCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC
ATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACATTTACATCACAACCCCTTGGAACTG
TAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCCGTG
TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTGCGGCCCTCCACATC
CCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGT
GCTCAGTGATGGTACGTTAAATTTACAAATGTAAGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCCTTTCTCTTACTTTTC
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCCCTCC
AGTGGTTCGACTGGGAGACCACCAATGTGAACACCTCTCTCACACCACAGGCACAAGGTGACAGAGAAAACCTT
CACCATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGATGAGGTGATGAAGACTACCAAAATCATCAT
TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGATGAGGAAGCAGCACC
TCGGCAAAACCATCACGCCCCAACAAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCAACAAATCTCCCTT
CAACCACACAACAACAGTTAACACAATAAAATTCATACACAGTTCAGTGCATGAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAAACAAACRATCAAAAAAAA
GACAGTTTATTAATAAATGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAA
AAAAGAAAAGAAATTTATTTATTAATAAATCTATTGTGATCTAAAGCAGACAAAAA

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FIGURE 368

MLNKMTLHPQQIMIGPRFNRALEDFLLVVLALQLLVVAGLVRAQTCPSVCSCSNQFSKVICVRKNLREVDPGIS
TNTRLLNLHENQIQIIKVNSEFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKL
KELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNRLRYLNLAMCNLREIPNLTPLIKLOELD
LSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLH
NPWNCNCDILWLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELKC
RASTSLTSVSWITFNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVNSVGNNTASATLNVTAATTT
FSYFSTVTVETMEPSQDEARTTDNNVGFTPVVDWETTNTVTSLTPOSTRSTEKFTTIPVTDINSGIPGIDEVMKT
TKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQNHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYS
YKSPFNHTTTVTNTINSIHSSVHEPLLIRMNSKDNVQETQI

Important features:**Signal sequence:**

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438, 442-446,
488-492, 606-610**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243, 391-397,
422-428, 433-439, 531-537

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FIGURE 369

CAAAACTTGGCGTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC
TGGGGGAGCGCGTTCCGGCTGTGGGGCGCCGCTCGGCBCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCTGGGTGGTCCCGTCCCTATCCCTCCTTTATATA
GAAACCTTCCACACTGGGAAGGCAGCGCGAGGCAGGAGGGCTCATGGTGAAGCAAGGAGGCGCGCTGATCTGCAG
GCGCACAGCATTCGGAGTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGCCTGGT
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGCCGGGTGCTGC
TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGCCGTGAGGGCCCCAGGATTTGGCCGAA
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTTGCGGAGGAGGAGCCGGTGTGGTACTGAGCCCTGAGG
AGCCCCGGGCTGCCAGCCGCGGCTCAGCTGCCCGGAGACTGTGCTGTTCAGGAGGGCGCTGCTGGACTGTG
GCGGTATTGACCTGCGTGAGTTCCCGGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAGAACCAACGAGC
TGGAAAAGATCTACCTGAGGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAAACAACCGCCTGA
CTTCCCGAGGGCTCCAGAGAAGGCGTTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC
TGACCTTGGCACCCCGCTTCTGCCAAACGCCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCT
ATGGGCTCACCTTTGGCCAGAAGCCAAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGGC
TGCCGGACAACATGTTC AACGGCTCCAGCAACGTCGAGGTCTCATCTGTCCAGCAACTTCTGCGCCACGTGC
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGGGGGCCT
TCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAACAACTACCTGACTGACGAGGGCCTGGACAACGAGA
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCAGCTGGGCTGC
CGCGCAGCTTGGTGTGCTGCACTTGGAGAGAAGCGCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCCACTGGCCTTCCAGGGCC
TCAAGCGGTTCACACGGTGCACCTGTACAACAACCGCTGGAGCGCGTGGCCAGTGGCCTGCCTCGCCGCGTGC
GCACCTCATGATCCTGCACAACAGATCACAGGCATTGGCCGCGAAGACTTTGCCACCACCTACTTCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACCAGCCACAGGTGCACCGCGACGCTTCCGCAAGCTGCGCCTGCTGC
GCTCGCTGGACCTGTGCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCTTGGCACGAGGGGCGCTGGCGGGCATGGCTCAGCTGCCTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCGCTGCCCTGGGTGGACCTCGCCCATCTGCAGCTGCTGGACA
TCGCGGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCGAGTCACTTGAGTACCTGTACCTGCAGAACACA
AGATTAGTGCGGTGCCCCGCAATGCCCTTCGACTCCACGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAAACAAGC
TGGCTGTGGGCTCCCTGCTGGACAGTGCCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGGCAACT
TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGGACTCTTTTCTGC
AGCACACGCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA
TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCCACGGCGTGTCCCACGGCCAGACACATGC
ACACACATCACACCTCAAACACCCAGCTCAGCCACACACAACCTACCTCCAAACCACCACAGTCTCTGTACAC
CCCCACTACCGCTGCCACGCCCTCTGAATCATGAGGGAAGGGTCTGCCCTGCCCTGGCACACACAGGCACCCA
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACCACACACACACATGCACAAGTCATGTGCGAA
CAGCCCTCCAAAGCCTATGCCACAGACAGCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCT
GTCCATCTGTCCGTCCGTCCCTGGAGAAGACACAAGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCCTCT
GGAACCTCACAAAAGCTGGCTTTTATTCTTTCCCATCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGCC
TGGCCACCCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACTTTTCCAATGGGCAAGCCCTAGTGGAGGCAGGATGGGAGAGCCCCCTGGGTGCTGCTGGGGCCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTTT
GTTCTTCAGGCCTGTGGGGGAAGTTCCGGGTGCCTTTATTTTATTCTTTCTAAGGAAAAAATGATAAAAT
CTCAAAGCTGATTTTTCTTGTATAGAAAACTAATATAAAGCATTATCCCTATCCCTGCAAAAAA

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FIGURE 370

MEGEEAEQPAWFHQWPWPGASDSAPPAGTMAQSRVLLLLLLLLLPPQLHLGPVLAVRAPGFGRSG
GHSLSPEENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVDCGGIDLREFPGDLPEH
TNHLSLQNNQLEKIYPEELSRLEHRLTLNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNKLT
APRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNVEVLI
LSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDNETFWK
LSSLEYLDLSSNNLSRVPA GLPRSLVLLHLEKNAIRSV DANVLTPIRSLEYLLHLSNQLREQG
IHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTL MILHNQITGIGREDFATTYFLEELNLS
YNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALARGALAGMA
QLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYLQNNKISAVP
ANAFDSTPNLKGIFLRFNKLAVGSVVD SAFRRLKHLQVLDIEGNLEFGDISKDRGLGKEKEE
EEEEEEEEEEETR

Important features:**Signal sequence:**

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554**Leucine zipper pattern.**amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

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FIGURE 371

CACTTTCTCCCTCTCTTCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGACCTCGGAGACCGCG
CCGGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTACCGCCCCCACCCTCCTCTTCTGCAC
TGCCGTCCTCCGGAAGACCTTTTCCCTGCTCTGTTCCTTCACCGAGTCTGTGCATCGCCCCGGACCTGGCCCG
GAGGAGGCTTGGCCCGCGGAGATGCTCTAGGGGCGGCGCGGAGGAGCGGCCGCGGGACGGAGGGCCCGGCAG
GAAGATGGGCTCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCCCTTTGCCTCTGGCCTGGTCTCT
GAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGCCGTGCTCTCCGGACCA
TGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCAGTCAGGACCAGGGGCTCCCTGCTTCCCGGTGCTT
GCGCTGCTGTGACCCCGGTACCTCCATGTACCCGGCGACCGCGGTGCCCCAGATCAACATCACTATCTTGAAAGG
GGAGAAGGGGTGACCCCGGAGATCGAGGCTTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCA
CACTGGACCCAAAGGGCAGAAGGGCTCCATGGGGGCCCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGCTTTTC
GGTGGGCGGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCGACACGGAGTTTCTGAACCT
CTACGACCACTTCAACATGTTTACCGGCAAGTTCTACTGCTACGTGCCCGGCTCTACTTCTTCAGCCTCAACGT
GCACACCTGGAACCAAGAGAGACCTACCTGCACATCATGAAGAACAGGAGGAGGTGGTGATCTTGTTGCGGCA
GGTGGGCGACCGCAGCATCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACG
CCTCTACAAGGGCGAACGTGAGAAGGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAGTGGCTACCT
GGTCAAGCACGCCACCGAGCCCCTAGCTGGCCGGCCACCTCCTTTCCTCTCGCCACCTTCCACCCCTGCGCTGTGC
TGACCCACCGCCTCTTCCCGGATCCCTGGACTCCGACTCCCTGGCTTTGGCATTCACTGAGACGCCCTGCACAC
ACAGAAAGCCAAAGCGATCGGTGCTCCAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCCAG
GGCGGGGACCCCGGAGAACCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGG
CGAGACGCGGGTGGCGGCAGGGCGTCCCAGGCTGCGGCACCGCGGCTCCAGTCTTGGAAATAATTAGGCAAAAT
CTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGGTTGTTATTTTTGTCTTTCCAGCCAG
CCTGCTGGCTCCCAAGAGAGAGGCTTTTTCAGTTGAGACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGG
GTCAGGGGAGGGGCGGGGGCAGGAACTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACCTTTCTTGAGGG
ATAGGTGGACCTGACATCCCTGTGGCTTGCCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGTGA
TGGGGGCTGGGGCCCCAGGCGTCAGCTTCCAGAGGGACAGCTGAGCCCCCTGCCTTGGCTCCAGGTGGTAGAA
GCAGCCGAAGGGCTCTTGACAGTGGCCAGGGACCCCTGGGTCCCCCAGGCTTGCAGATGTTTCTATAGGGGGCAG
AGCTCCTTGGTACATCCATGTGTGGCTCTGCTCCACCCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATG
CCTGCCACCTGGCATCGGCTTTCTGTGCGGCTTCCACACAAATCAGCCCCAGAAGSCCCGGGGCCTTGGCTT
CTGTTTTTTATAAAACACCTCAAGCAGCAC'TGCAGTCTCCCATCTCCTCGTGGGCTAAGCATCACCGCTTCCACG
TGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCTCATCCAGGCTCTGACCA
GTAGCCTGAGAGGGGCTTTTCTAGGCTTCAGAGCAGGGGAGAGCTGGAAGGGGCTAGAAAGCTCCCGCTTGTCT
GTTTCTCAGGCTCCTGTGAGCCTCAGTCCCTGAGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCGTGTCA
GGATTCACTCTCAGGAGCTGGGTGGCAGGAGAGGCAATAGCCCCGTGTGGCAATTGCAGGACCAGCTGGAGCAGGG
TTGCGGTGTCTCCACGGTGTCTCGCCCTGCCATGGCCACCCACAGACTCTGATCTCCAGGAACCCCATAGCCCC
TCTCCACCTCACCCCATGTTGATGCCCAGGGTCAC'PCTTGCTACCCGCTGGGCCCCCAAACCCCGCTGCCTCTC
TTCCTTCCCCCATCCCCACCTGGT'TTTGACTAATCCTGCTTCCCTCTCTGGGCTGGCTGCCGGGATCTGGGG
TCCCTAAGTCCCTCTCTTTAAAGAACTTCTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAG
CAGAGCGCCACACTCGCTGCTTAAGCTCCCCCAGCTCTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

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FIGURE 372

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRPS
QDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGHTG
PKGQKGSMPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMTGKFYCYV
PGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWVRLYK
GERENAI FSEELDTYITFSGYLVKHATEP

Important features:**Signal sequence.**

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

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FIGURE 373

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCCG
TTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGAA
GCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAATGC
ACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTTCAGAGG
ATGAGCGCATGGAGCTCAGTAAGAGCTTTTCGAGTATACTGTATTATCCTTGTAACCCCAAAG
ATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACTGTGACAAAGCAGAGTTCT
TCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTAATATGGACACAAATGACATGTGGTTAA
TGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACCTGGTTCTTCC
TTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTTAAAAAAGGATC
CATCACAGCCTTTCATCTAGGCCACACTATAAAATCTGGAGACCTTGAATATGTGGGTATGG
AAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCTCAATATCCCAG
AAAAGTGTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAACAGCTAGCAGTTT
GCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGAAAAGATGTATTTA
ATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCCCAACCAGGTAGTAG
AAGGCTGTTGTTTCAGATATGGCTGTTACTTTTAATGGACTGACTCCAAATCAGATGCATGTGA
TGATGTATGGGGTATACCGCCTTAGGGCATTGTTGGGCATATTTCAATGATGCATTGGTTTTCT
TACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCGTGAATATGATCTTTGTA
TAGGACGTGTGTTGTCATTATTTGTAGTAGTAACTACATATCCAATACAGCTGTATGTTTCTT
TTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAGTCAGTAGTACATTTTTAAA
TGAGGGTGGTTTTTTTCTTTAAACACATGAACATTGTAAATGTGTTGGAAAGAAGTGTTTTA
AGAATAATAATTTGCAAATAAACTATTAATAAATATTATATGTGATAAATTCTAAATTATGA
ACATTAGAAATCTGTGGGGCACATATTTTGTCTGATTGGTTAAAAAATTTTAACAGGTCTTTA
GCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATTTGTGATTAAAGTAAACCTTTTAG
CTGTGTGTTCCCTTACTTCTAATACTGATTTATGTTCTAAGCCTCCCCAAGTTCCAATGGAT
TTGCCTTCTCAAATGTACAATAAGCAACTAAAGAAAATTAAAGTGAAAGTTGAAAAAT

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FIGURE 374

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHEHHHLQAPNKEDILKISEDERMELSKSFRVYCIILV
RPKDVSLWAAVKETWTKHCDKAEFFSSSENVKVFESINMDTNDMWLMMRKAYKYAFDKYRDQYNWFFLARPTTFAI
IENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAV
CLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFG
HIFNDALVFLPPNGSDND

Important features:**Signal sequence:**

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389, 399-403,
409-413, 473-477, 729-733, 748-752**Tyrosine kinase phosphorylation site.**

amino acids 736-743

N-myristoylation site.amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550, 558-564,
651-657, 657-663, 672-672**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

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FIGURE 375

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAAT
CTATCAGGAAAGAAAGAAAGAAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGAA
AAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCACGGG
GCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCCCCAA
AGCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCCTCAGGTGCACTATTGACAA
CCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTG
GTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCGAGATCCA
GAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAACCACCCAAA
GACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAATTGTAGAGATTTCTTCAGATAT
CTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTAC
GGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGA
AATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGC
CGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATAACATTTCAGAAGCCAA
GGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCTC
AGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGT
GGAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAA
CTACACTTGCCTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCC
AGGCGCCGTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCGTCTGGCTGCTGCC
TCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCCACTTCCCCACCCGGGAAAG
GCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACACCGACAGCAACCAATCAGATA
TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAACAAA
GAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAAAATTGCCTTGCAGATATTTAGG
TACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGCACACCCGGCTTGGACCCACTGCA
AGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCCACAGA
GTGCCCCCAGTGGAACATTCTGGAGCTGGCCATCCCAAATTCAATCAGTCCATAGAGACGAA
CAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGGGCACTTTGGTAGACTGTGCCACCACG
GCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAAAAAA

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FIGURE 376

MKTIQPKMHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNRV
TRVAWLNIRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVVDVYDEGPYTCVQTDNHPKTS
RVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYLEIQ
GITREQSGDYECASNDVAAPVRRVKVTVNYPPISEAKGTGVPVGQKGTLOCEASAVPSAE
FQWYKDDKRLIEGKKGKVENRPFLSKLIFFNVSEHDYGNVTCVASNKLGHTNASIMLFGPGA
VSEVSNGTSRRAGCVWLLPLLVLHLLLKF

Important features:**Signal peptide:**

amino acids 1-28

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FIGURE 377

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCCCTTTAGATTGTGAA
ATGTGGCTCAAGGTCTTCACAACCTTTCCTTTTCTTTGCAACAGGTGCTTGCTCGGGGCTGAAG
GTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTCAC
TATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCACACA
ATGCCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACCAACAC
AAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTTGATGAA
GGCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAAGTCTATCTGCCAGTCAGAAGATA
CAAGTCACGGTTGATGATCCTGTCACAAAGCCAGTGGTGCAGATTCATCCTCCCTCTGGGGCT
GTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGGCTAGCTTAC
CAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTCTCCCCAAAC
AATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCTGCCTGGTGAGG
AACCCTGTCAGTGAAATGGAAAGTGATATCATTATGCCCATCATATATTATGGACCTTATGGA
CTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGTTGACCTTGAGAG
GCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACTCCTGGATTAGGAGG
ACTGACAATACTACATATATCATTAAGCATGGGCCCTCGCTTAGAAGTTGCATCTGAGAAAGTA
GCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAACCGGCAGGCAAGATGAA
ACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTGCACAGAAAGGAAAATCA
TTGTCACCTTTAGCAAGTATAACTGGAATATCACTATTTTTTGATTATATCCATGTGTCTTCTC
TTCCTATGGAAAAAATATCAACCCTACAAAGTTATAAAACAGAACTAGAAGGCAGGCCAGAA
ACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATGCTCTGGATGACTTCGGAATA
TATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGGATTCCAAGCAGGTCTGTTCCA
GCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGTGTATGAAGTTATTCAGCACATC
CCTGCCCAGCAGCAAGACCATCCAGAG**TGA**ACTTTTCATGGGCTAAACAGTACATTCGAGTGAA
ATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAGTATATTAATCTGGAATCAGTGAAGA
AACCAGGACCAACACCTCTTACTCATTATTCCTTTACATGCAGAATAGAGGCATTTATGCAAA
TTGAAGTGCAGGTTTTTTCAGCATATACACAATGTCTTGTGCAACAGAAAAACATGTTGGGGAA
ATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGGGGAGAACGAAAGTGACAGGGGTTTTCT
CATAAGTTTTGTATGAAATATCTCTACAAACCTCAATTAGTTCTACTCTACACTTTCACTATC
ATCAACACTGAGACTATCCTGTCTCACCTACAAATGTGGAACTTTACATTGTTTCGATTTTTTC
AGCAGACTTTGTTTTATTAATTTTTTATTAGTGTTAAGAATGCTAAATTTATGTTTCAATTTT
ATTTCCAAATTTCTATCTTGTTATTTGTACAACAAAGTAATAAGGATGGTTGTCACAAAAACA
AACTATGCCTTCTCTTTTTTTTCAATCACCAGTAGTATTTTTGAGAAGACTTGTGAACACTT
AAGGAAATGACTATTAAAGTCTTATTTTTTATTTTTTTCAAGGAAAGATGGATTCAAATAAAT
ATTCTGTTTTTGCTTTTAAAAAAAAAAAAAA